RAW SEQUENCE LISTING ERROR REPORT

3500

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable

Application Serial Number: **09/869,004**

Source: **PCT/09**

Date Processed by STIC: **7/9/2001**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT WITH A NOTICE TO COMPLY, or
2) CONTACTING THE APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.
IF YOU HAVE ANY QUESTIONS, PLEASE CONTACT MARK SPENGLER, 703-308-1212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/869,004

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces

3 ____ Misaligned Amino
Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers, use space characters, instead

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X. (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences

8 ____ Skipped Sequences
(NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ____ Invalid <213>
Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ✓ ____ PatentIn 2.0
"bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/869,004

DATE: 07/09/2001
TIME: 10:11:50

Input Set : A:\Ru-0076.app
Output Set: N:\CRF3\07092001\I869004.raw

```
C--> 3 <140> CURRENT APPLICATION NUMBER: US/09/869,004
C--> 3 <141> CURRENT FILING DATE: 2001-06-22
W--> 0 <110> APPLICANT:
W--> 0 <120> TITLE INVENTION:
W--> 0 <130> FILE REFERENCE:
     3 <150> PRIOR APPLICATION NUMBER: 60/113,731
     4 <151> PRIOR FILING DATE: 1998-12-23
     6 <160> NUMBER OF SEQ ID NOS: 3
     8 <170> SOFTWARE: PatentIn Ver. 2.0
    10 <210> SEQ ID NO: 1
    11 <211> LENGTH: 13
    12 <212> TYPE: DNA
    13 <213> ORGANISM: Artificial Sequence
    15 <220> FEATURE:
    16 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    18 <400> SEQUENCE: 1
    19 gcgtacatgt gcg                                                      13
    21 <210> SEQ ID NO: 2
    22 <211> LENGTH: 13
    23 <212> TYPE: DNA
    24 <213> ORGANISM: Artificial Sequence
    26 <220> FEATURE:
    27 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    29 <400> SEQUENCE: 2
    30 gcatgtgta cgc                                                       13
    32 <210> SEQ ID NO: 3
    33 <211> LENGTH: 13
    34 <212> TYPE: DNA
    35 <213> ORGANISM: Artificial Sequence
    37 <220> FEATURE:
    38 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    39      n=basi: furan
    41 <220> FEATURE:
    42 <221> NAME/KEY: misc_feature
    43 <222> LOCATION: (7)
    45 <400> SEQUENCE: 3
W--> 46 cgcatgngta cgc                                                     13
```

see next page

Does Not Comply
Corrected Diskette Needed

Delete

Explanation for "n" or "Xaa" goes on its own

<2237 line.

< 2237

FYI: "n" can only represent a single nucleotide (base) nothing else

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/869,004**

DATE: 07/09/2001
TIME: 10:11:51

Input Set : **A:\Ru-0076.app**
Output Set: **N:\CRF3\07092001\I869004.raw**

L:3 M:270 C: Current Application Number differs, Replaced Current Application No
L:3 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3